



-1-

SEQUENCE LISTING

<110> Gardella, Thomas J.
Kronenberg, Henry M.
Potts, John T.
Juppner, Harald

<120> PTH Functional Domain Conjugate Peptides, Derivatives
Thereof and Novel Tethered Ligand-Receptor Molecules

<130> 0609.4780001

<140> US 09/475,158

<141> 1999-12-30

<150> US 60/114,577

<151> 1998-12-31

<160> 74

<170> PatentIn Ver. 2.1

<210> 1

<211> 9

<212> PRT

<213> Homo sapiens

<400> 1

Ala Val Ser Glu Ile Gln Leu Met His
1 5

<210> 2

<211> 17

<212> PRT

<213> Homo sapiens

<400> 2

Leu Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp
1 5 10 15

Val

<210> 3

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> modified PTH sequence

<400> 3

Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Leu Asn
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val

20

25

30

<210> 4
<211> 5
<212> PRT
<213> Homo sapiens

<400> 4
Ala Val Ser Glu Ile
1 5

<210> 5
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> modified PTH sequence

<400> 5

Ala Val Ser Glu Ile Gly Gly Gly Gly Gly Gly Gly Gly Gly Leu Asn
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 6
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> modified PTH sequence

<400> 6

Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 7
<211> 9
<212> PRT
<213> Homo sapiens

<400> 7
Ala Val Ser Glu His Gln Leu Leu His
1 5

<210> 8
<211> 17

<212> PRT
<213> Homo sapiens

<400> 8
Ile Gln Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu
1 5 10 15
Ile

<210> 9
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> modified PTH sequence

<220>
<221> MOD_RES
<222> (31)..(31)
<223> AMIDATION

<400> 9

Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Leu Asn
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 10
<211> 5
<212> PRT
<213> Homo sapiens

<400> 10
Ala Val Ser Glu His
1 5

<210> 11
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> modified PTH sequence

<220>
<221> MOD_RES
<222> (31)..(31)
<223> AMIDATION

<400> 11

-4-

Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
 20 25 30

<210> 12
<211> 15
<212> PRT
<213> Homo sapiens

<400> 12
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
1 5 10 15

<210> 13
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> modified PTH sequence

<220>
<221> MOD_RES
<222> (31)..(31)
<223> AMIDATION

<400> 13

Ala Val Ser Glu Ile Gly Gly Gly Gly Gly Gly Gly Gly Gly Leu Asn
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
 20 25 30

<210> 14
<211> 93
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 14
gcuguuuccg aaauccagcu gaugcacggu ggugguggug gucugaacuc cauggaacgu 60
guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 15
<211> 93

<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 15
gcuguuuccg aaauccagcu gaugcacggu ggugguggug guggugguuc cauggaacgu 60
guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 16
<211> 93
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 16
gcuguuuccg aaauccggugg uggugguggu ggugguggug gucugaacuc cauggaacgu 60
guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 17
<211> 34
<212> PRT
<213> Homo sapiens

<400> 17
Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn
1 5 10 15
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His
20 25 30

Asn Phe

<210> 18
<211> 34
<212> PRT
<213> Homo sapiens

<400> 18
Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly Lys Ser Ile Gln
1 5 10 15
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile His
20 25 30

Thr Ala

<210> 19
<211> 37
<212> PRT
<213> Homo sapiens

<400> 19
His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln
1 5 10 15
Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu Gly Lys Arg Tyr Lys
20 25 30
Gln Arg Val Asn Lys
35

<210> 20
<211> 28
<212> PRT
<213> Homo sapiens

<400> 20
His Ser Asp Ala Val Phe Thr Asp Asn Tyr Thr Arg Leu Arg Lys Gln
1 5 10 15
Met Ala Val Lys Lys Tyr Leu Asn Ser Ile Leu Asn
20 25

<210> 21
<211> 29
<212> PRT
<213> Homo sapiens

<400> 21
Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
1 5 10 15
Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg
20 25

<210> 22
<211> 27
<212> PRT
<213> Homo sapiens

<400> 22
His Ala Asp Gly Val Phe Thr Ser Asp Phe Ser Lys Leu Leu Gly Gln
1 5 10 15
Leu Ser Ala Lys Lys Tyr Leu Glu Ser Leu Met
20 25

<210> 23
<211> 31
<212> PRT
<213> Homo sapiens

<400> 23
His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15
Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
20 25 30

<210> 24
 <211> 29
 <212> PRT
 <213> Homo sapiens

<400> 24
 His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Ser
 1 5 10 15
 Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
 20 25

<210> 25
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 25
 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys
 1 5 10 15
 Ile His Gln Gln Asp Phe Val Asn Trp Leu Leu Ala Gln Lys Gly Lys
 20 25 30
 Lys Asn Asp Trp Lys His Asn Ile Thr Gln
 35 40

<210> 26
 <211> 27
 <212> PRT
 <213> Homo sapiens

<400> 26
 His Ser Asp Gly Thr Phe Thr Ser Glu Leu Ser Arg Leu Arg Glu Gly
 1 5 10 15
 Ala Arg Leu Gln Arg Leu Leu Gln Gly Leu Val
 20 25

<210> 27
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 27
 Cys Gly Asn Leu Ser Thr Cys Met Leu Gly Thr Tyr Thr Gln Asp Phe
 1 5 10 15
 Asn Lys Phe His Thr Phe Pro Gln Thr Ala Ile Gly Val Gly Ala Pro
 20 25 30

<210> 28
 <211> 37
 <212> PRT

<213>Homo sapiens

<400> 28

Ala Cys Asn Thr Ala Thr Cys Val Thr His Arg Leu Ala Gly Leu Leu
1 5 10 15

Ser Arg Ser Gly Gly Met Val Lys Ser Asn Phe Val Pro Thr Asn Val
20 25 30

Gly Ser Lys Ala Phe
35

<210> 29

<211> 37

<212> PRT

<213> Homo sapiens

<400> 29

Ala Cys Asp Thr Ala Thr Cys Val Thr His Arg Leu Ala Gly Leu Leu
1 5 10 15

Ser Arg Ser Gly Gly Val Val Lys Asn Asn Phe Val Pro Thr Asn Val
20 25 30

Gly Ser Lys Ala Phe
35

<210> 30

<211> 37

<212> PRT

<213>Homo sapiens

<400> 30

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

<210> 31

<211> 36

<212> PRT

<213> Homo sapiens

<400> 31

Gly Cys Arg Phe Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile
1 5 10 15

Tyr Gln Phe Thr Asp Lys Asp Lys Asp Asn Val Ala Pro Arg Ser Lys
20 25 30

Ile Ser Pro Gln
35

<210> 32

<211> 41
<212> PRT
<213> Homo sapiens

<400> 32
Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg
1 5 10 15
Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His
20 25 30
Ser Asn Arg Lys Leu Met Glu Ile Ile
35 40

<210> 33
<211> 40
<212> PRT
<213> Homo sapiens

<400> 33
Glu Glu Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys
1 5 10 15
Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala Ala Asn
20 25 30
Asn Arg Leu Leu Asp Thr Ile
35 40

<210> 34
<211> 46
<212> PRT
<213> Homo sapiens

<400> 34
Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg
1 5 10 15
Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln
20 25 30
Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile
35 40 45

<210> 35
<211> 63
<212> PRT
<213> Homo sapiens

<400> 35
Cys Asp Ala Thr Cys Gln Phe Arg Lys Ala Ile Asp Asp Cys Gln Lys
1 5 10 15
Gln Ala His His Ser Asn Val Leu Gln Thr Ser Val Gln Thr Thr Ala
20 25 30
Thr Phe Thr Ser Met Asp Thr Ser Gln Leu Pro Gly Asn Ser Val Phe
35 40 45

Lys Glu Cys Met Lys Gln Lys Lys Lys Glu Phe Ser Ser Gly Lys
50 55 60

<210> 36
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<220>
<221> CDS
<222> (1)..(1332)

<400> 36
atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc 48
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
1 5 10 15
cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga 96
Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
20 25 30
gga ggc gag gta ttt gac cgc cta ggc atg atc tac acc gtg gga tac 144
Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
35 40 45
tcc atg tct ctc gcc tcc ctc acg gtg gct gtg ctc atc ctg gcc tat 192
Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
50 55 60
ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac atg ttc 240
Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe
65 70 75 80
ctg tcg ttt atg ctg cgc gcc gcg agc atc ttc gtg aag gac gct gtg 288
Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val
85 90 95
ctc tac tct ggc ttc acg ctg gat gag gcc gag cgc ctc aca gag gaa 336
Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu
100 105 110
gag ttg cac atc atc gcg cag gtg cca cct ccg ccg gcc gct gcc gcc 384
Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala Ala
115 120 125
gta ggc tac gct ggc tgc cgc gtg gcg gtg acc ttc ttc ctc tac ttc 432
Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe
130 135 140
ctg gct acc aac tac tac tgg atc ctg gtg gag ggg ctg tac ttg cac 480
Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His
145 150 155 160
agc ctc atc ttc atg gcc ttt ttc tca gag aag aag tac ctg tgg ggc 528
Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly
165 170 175

ttc acc atc ttt ggc tgg ggt cta ccg gct gtc ttc gtg gct gtg tgg	576
Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp	
180 185 190	
gtc ggt gtc aga gca acc ttg gcc aac act ggg tgc tgg gat ctg agc	624
Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser	
195 200 205	
tcc ggg cac aag aag tgg atc atc cag gtg ccc atc ctg gca tct gtt	672
Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val	
210 215 220	
gtg ctc aac ttc atc ctt ttt atc aac atc atc cgg gtg ctt gcc act	720
Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr	
225 230 235 240	
aag ctt cgg gag acc aat gcg ggc cgg tgt gac acc agg cag cag tac	768
Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr	
245 250 255	
cgg aag ctg ctc agg tcc acg ttg gtg ctc gtg ccg ctc ttt ggt gtg	816
Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val	
260 265 270	
cac tac acc gtc ttc atg gcc ttg ccg tac acc gag gtc tca ggg aca	864
His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr	
275 280 285	
ttg tgg cag atc cag atg cat tat gag atg ctc ttc aac tcc ttc cag	912
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln	
290 295 300	
gga ttt ttt gtt gcc atc ata tac tgt ttc tgc aat ggt gag gtg cag	960
Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln	
305 310 315 320	
gca gag att agg aag tca tgg agc cgc tgg aca ctg gcg ttg gac ttc	1008
Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe	
325 330 335	
aag cgc aaa gca cga agt ggg agt agc agc tac agc tat ggc cca atg	1056
Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met	
340 345 350	
gtg tct cac acg agt gtg acc aat gtg ggc ccc cgt gca gga ctc agc	1104
Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser	
355 360 365	
ctc ccc ctc agc ccc cgc ctg cct cct gcc act acc aat ggc cac tcc	1152
Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser	
370 375 380	
cag ctg cct ggc cat gcc aag cca ggg gct cca gcc act gag act gaa	1200
Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu	
385 390 395 400	
acc cta cca gtc act atg gcg gtt ccc aag gac gat gga ttc ctt aac	1248
Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn	
405 410 415	
ggc tcc tgc tca ggc ctg gat gag gag gcc tcc ggg tct gcg cgg ccg	1296
Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser Ala Arg Pro	

420	425	430	
cct cca ttg ttg cag gaa gga tgg gaa aca gtc atg tga			1335
Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met			
435	440		

<210> 37
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 37
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
 20 25 30
 Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 35 40 45
 Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
 50 55 60
 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe
 65 70 75 80
 Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val
 85 90 95
 Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu
 100 105 110
 Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala
 115 120 125
 Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe
 130 135 140
 Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His
 145 150 155 160
 Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly
 165 170 175
 Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp
 180 185 190
 Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser
 195 200 205
 Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val
 210 215 220
 Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr
 225 230 235 240
 Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr
 245 250 255
 Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val
 260 265 270
 His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr
 275 280 285
 Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln
 290 295 300
 Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln
 305 310 315 320
 Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe
 325 330 335
 Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met
 340 345 350

```

Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser
      355                      360                      365
Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser
      370                      375                      380
Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu
385                      390                      395                      400
Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn
      405                      410                      415
Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser Ala Arg Pro
      420                      425                      430
Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met
      435                      440

```

<210> 38
 <211> 1002
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(1002)

```

<400> 38
atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc 48
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
      1                      5                      10                      15

cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga 96
Pro Val Leu Ser Ser Ala Tyr Ala Glu Thr Ser Glu His Gly Gly
      20                      25                      30

gga ggc gag gta ttt gac cgc cta ggc atg atc tac acc gtg gga tac 144
Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
      35                      40                      45

tcc atg tct ctc gcc tcc ctc acg gtg gct gtg ctc atc ctg gcc tat 192
Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
      50                      55                      60

ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac atg ttc 240
Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe
      65                      70                      75                      80

ctg tcg ttt atg ctg cgc gcc gcg agc atc ttc gtg aag gac gct gtg 288
Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val
      85                      90                      95

ctc tac tct ggc ttc acg ctg gat gag gcc gag cgc ctc aca gag gaa 336
Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu
      100                      105                      110

gag ttg cac atc atc gcg cag gtg cca cct ccg ccg gcc gct gcc gcc 384
Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala Ala
      115                      120                      125

gta ggc tac gct ggc tgc cgc gtg gcg gtg acc ttc ttc ctc tac ttc 432

```

Val	Gly	Tyr	Ala	Gly	Cys	Arg	Val	Ala	Val	Thr	Phe	Phe	Leu	Tyr	Phe		
130						135					140						
ctg	gct	acc	aac	tac	tac	tgg	atc	ctg	gtg	gag	ggg	ctg	tac	ttg	cac	480	
Leu	Ala	Thr	Asn	Tyr		Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His		
145					150					155					160		
agc	ctc	atc	ttc	atg	gcc	ttt	ttc	tca	gag	aag	aag	tac	ctg	tgg	ggc	528	
Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	Glu	Lys	Lys	Tyr	Leu	Trp	Gly		
				165					170					175			
ttc	acc	atc	ttt	ggc	tgg	ggt	cta	ccg	gct	gtc	ttc	gtg	gct	gtg	tgg	576	
Phe	Thr	Ile	Phe	Gly	Trp	Gly	Leu	Pro	Ala	Val	Phe	Val	Ala	Val	Trp		
			180					185						190			
gtc	ggt	gtc	aga	gca	acc	ttg	gcc	aac	act	ggg	tgc	tgg	gat	ctg	agc	624	
Val	Gly	Val	Arg	Ala	Thr	Leu	Ala	Asn	Thr	Gly	Cys	Trp	Asp	Leu	Ser		
		195					200					205					
tcc	ggg	cac	aag	aag	tgg	atc	atc	cag	gtg	ccc	atc	ctg	gca	tct	gtt	672	
Ser	Gly	His	Lys	Lys	Trp	Ile	Ile	Gln	Val	Pro	Ile	Leu	Ala	Ser	Val		
	210					215				220							
gtg	ctc	aac	ttc	atc	ctt	ttt	atc	aac	atc	atc	cgg	gtg	ctt	gcc	act	720	
Val	Leu	Asn	Phe	Ile	Leu	Phe	Ile	Asn	Ile	Ile	Arg	Val	Leu	Ala	Thr		
225					230					235					240		
aag	ctt	cgg	gag	acc	aat	gcg	ggc	cgg	tgt	gac	acc	agg	cag	cag	tac	768	
Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	Cys	Asp	Thr	Arg	Gln	Gln	Tyr		
				245				250						255			
cgg	aag	ctg	ctc	agg	tcc	acg	ttg	gtg	ctc	gtg	ccg	ctc	ttt	ggt	gtg	816	
Arg	Lys	Leu	Leu	Arg	Ser	Thr	Leu	Val	Leu	Val	Pro	Leu	Phe	Gly	Val		
			260					265						270			
cac	tac	acc	gtc	ttc	atg	gcc	ttg	ccg	tac	acc	gag	gtc	tca	ggg	aca	864	
His	Tyr	Thr	Val	Phe	Met	Ala	Leu	Pro	Tyr	Thr	Glu	Val	Ser	Gly	Thr		
		275					280					285					
ttg	tgg	cag	atc	cag	atg	cat	tat	gag	atg	ctc	ttc	aac	tcc	ttc	cag	912	
Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	Met	Leu	Phe	Asn	Ser	Phe	Gln		
	290					295				300							
gga	ttt	ttt	gtt	gcc	atc	ata	tac	tgt	ttc	tgc	aat	ggt	gag	gtg	cag	960	
Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	Phe	Cys	Asn	Gly	Glu	Val	Gln		
305					310					315					320		
gca	gag	att	agg	aag	tca	tgg	agc	cgc	tgg	aca	ctg	gcg	tag			1002	
Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	Trp	Thr	Leu	Ala					
				325					330								

<210> 39

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH
receptor sequence

```

<400> 39
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1          5          10          15
Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
 20          25          30
Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 35          40          45
Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
 50          55          60
Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe
 65          70          75          80
Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val
 85          90          95
Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu
100          105          110
Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala Ala
115          120          125
Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe
130          135          140
Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His
145          150          155          160
Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly
165          170          175
Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp
180          185          190
Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser
195          200          205
Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val
210          215          220
Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr
225          230          235          240
Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr
245          250          255
Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val
260          265          270
His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr
275          280          285
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln
290          295          300
Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln
305          310          315          320
Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala
          325          330

```

```

<210> 40
<211> 975
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: modified PTH
      receptor sequence

```

```

<220>
<221> CDS
<222> (1)..(972)

```

```

<400> 40
atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys

```

48

1	5	10	15	
cca gtg ctc agc tcc gca tat gcg ctg gag gta ttt gac cgc cta ggc	96			
Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly				
20 25 30				
atg atc tac acc gtg gga tac tcc atg tct ctc gcc tcc ctc acg gtg	144			
Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val				
35 40 45				
gct gtg ctc atc ctg gcc tat ttt agg cgg ctg cac tgc acg cgc aac	192			
Ala Val Leu Ile Leu Ala Phe Arg Arg Leu His Cys Thr Arg Asn				
50 55 60				
tac atc cac atg cac atg ttc ctg tcg ttt atg ctg cgc gcc gcg agc	240			
Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser				
65 70 75 80				
atc ttc gtg aag gac gct gtg ctc tac tct ggc ttc acg ctg gat gag	288			
Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu				
85 90 95				
gcc gag cgc ctc aca gag gaa gag ttg cac atc atc gcg cag gtg cca	336			
Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro				
100 105 110				
cct ccg ccg gcc gct gcc gcc gta ggc tac gct ggc tgc cgc gtg gcg	384			
Pro Pro Pro Ala Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala				
115 120 125				
gtg acc ttc ttc ctc tac ttc ctg gct acc aac tac tac tgg atc ctg	432			
Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu				
130 135 140				
gtg gag ggg ctg tac ttg cac agc ctc atc ttc atg gcc ttt ttc tca	480			
Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser				
145 150 155 160				
gag aag aag tac ctg tgg ggc ttc acc atc ttt ggc tgg ggt cta ccg	528			
Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro				
165 170 175				
gct gtc ttc gtg gct gtg tgg gtc ggt gtc aga gca acc ttg gcc aac	576			
Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn				
180 185 190				
act ggg tgc tgg gat ctg agc tcc ggg cac aag aag tgg atc atc cag	624			
Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln				
195 200 205				
gtg ccc atc ctg gca tct gtt gtg ctc aac ttc atc ctt ttt atc aac	672			
Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn				
210 215 220				
atc atc cgg gtg ctt gcc act aag ctt cgg gag acc aat gcg ggc cgg	720			
Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg				
225 230 235 240				
tgt gac acc agg cag cag tac cgg aag ctg ctc agg tcc acg ttg gtg	768			
Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val				
245 250 255				

ctc	gtg	ccg	ctc	ttt	ggg	gtg	cac	tac	acc	gtc	ttc	atg	gcc	ttg	ccg	816
Leu	Val	Pro	Leu	Phe	Gly	Val	His	Tyr	Thr	Val	Phe	Met	Ala	Leu	Pro	
			260					265					270			
tac	acc	gag	gtc	tca	ggg	aca	ttg	tgg	cag	atc	cag	atg	cat	tat	gag	864
Tyr	Thr	Glu	Val	Ser	Gly	Thr	Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	
		275					280					285				
atg	ctc	ttc	aac	tcc	ttc	cag	gga	ttt	ttt	gtt	gcc	atc	ata	tac	tgt	912
Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	
	290					295					300					
ttc	tgc	aat	ggg	gag	gtg	cag	gca	gag	att	agg	aag	tca	tgg	agc	cgc	960
Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	
305					310					315					320	
tgg	aca	ctg	gcg	tag												975
Trp	Thr	Leu	Ala													

<210> 41
 <211> 324
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 41
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly
 20 25 30
 Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val
 35 40 45
 Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn
 50 55 60
 Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser
 65 70 75 80
 Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu
 85 90 95
 Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro
 100 105 110
 Pro Pro Pro Ala Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala
 115 120 125
 Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu
 130 135 140
 Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser
 145 150 155 160
 Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro
 165 170 175
 Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn
 180 185 190
 Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln
 195 200 205
 Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn
 210 215 220
 Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
 225 230 235 240
 Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val

				245					250					255		
Leu	Val	Pro	Leu	Phe	Gly	Val	His	Tyr	Thr	Val	Phe	Met	Ala	Leu	Pro	
			260					265					270			
Tyr	Thr	Glu	Val	Ser	Gly	Thr	Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	
		275					280					285				
Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	
	290					295					300					
Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	
305					310					315					320	
Trp	Thr	Leu	Ala													

<210> 42
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)..(1)
 <223> May be any amino acid.

<220>
 <221> UNSURE
 <222> (3)..(3)
 <223> May be any amino acid.

<220>
 <221> UNSURE
 <222> (5)..(8)
 <223> May be any amino acid.

<220>
 <223> Description of Artificial Sequence: synthetic polypeptide

<400> 42
 Xaa Val Xaa Glu Xaa Xaa Xaa Xaa His
 1 5

<210> 43
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)..(5)
 <223> May be any amino acid.

<220>
 <221> UNSURE
 <222> (7)..(8)
 <223> May be any amino acid.

<220>
 <221> UNSURE
 <222> (10)
 <223> May be any amino acid.

<220>
 <221> UNSURE
 <222> (12)
 <223> May be any amino acid.

<220>
 <221> UNSURE
 <222> (15)..(16)
 <223> May be any amino acid.

<220>
 <223> Description of Artificial Sequence: synthetic
 Polypeptide

<400> 43
 Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Trp Xaa Leu Xaa Lys Leu Xaa Xaa
 1 5 10 15

Val

<210> 44
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 44
 Ser Val Ser Glu Ile Gln Leu Met His
 1 5

<210> 45
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 45
 Leu Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln
 1 5 10 15

Asp Val

<210> 46
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(120)

<400> 46
 atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15

cca gtg ctc agc tcc gca tat gcg ctg gtg gat gcg gac gat gtc ttt 96
Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Phe
20 25 30

acc aaa gag gaa cag att ttc ctg 120
Thr Lys Glu Glu Gln Ile Phe Leu
35 40

<210> 47
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<220>
<221> CDS
<222> (1)..(120)

<400> 47 48
aac cgg acg tgg gcc aac tac agc gag tgc ctc aag ttc atg acc aat
Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn
1 5 10 15

gag acc cgg gaa cgg gag gta ttt gac cgc cta ggc atg atc tac acc 96
Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
20 25 30

gtg gga tac tcc atg tct ctc gcc 120
Val Gly Tyr Ser Met Ser Leu Ala
35 40

<210> 48
<211> 39
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 48 39
gcuguuuccg aaauccagcu gaugcacggc ggaggaggc

<210> 49
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 49 60
ctctgctgcc cagtgtctcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 99
ggaggaggcg aggtatttga ccgcctaggc atgatctac

<210> 50
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> modified PTH receptor sequence

<220>
 <221> misc_feature
 <222> (1)..(30)
 <223> flanking region

<220>
 <221> misc_feature
 <222> (31)..(69)
 <223> insert

<220>
 <221> misc_feature
 <222> (70)..(99)
 <223> flanking region

<220>
 <221> CDS
 <222> (1)..(99)

<400> 50		
ctc tgc tgc cca gtg ctc agc tcc gcc tat gcg gtt tcc gaa atc cag		48
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln		
1 5 10 15		
ctg atg cac ggc gga gga ggc gag gta ttt gac cgc cta ggc atg atc		96
Leu Met His Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile		
20 25 30		
tac		99
Tyr		

<210> 51
 <211> 96
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 51		
ctctgctgcc cagtgtcag ctccgcatat ccctacgacg tccccgacta cgccggcgga	60	
ggaggcgagg tatttgaccg cctaggcatg atctac	96	

<210> 52
 <211> 96
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<220>
<221> misc_feature
<222> (28)..(54)
<223> insert

<220>
<221> CDS
<222> (1)..(96)

<400> 52
ctc tgc tgc cca gtg ctc agc tcc gca tat ccc tac gac gtc ccc gac 48
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Pro Tyr Asp Val Pro Asp
1 5 10 15

tac gcc ggc gga gga ggc gag gta ttt gac cgc cta ggc atg atc tac 96
Tyr Ala Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
20 25 30

<210> 53
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 53
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
1 5 10 15

Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Phe
20 25 30

Thr Lys Glu Glu Gln Ile Phe Leu
35 40

<210> 54
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 54
Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn
1 5 10 15

Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
20 25 30

Val Gly Tyr Ser Met Ser Leu Ala
35 40

<210> 55
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 55
 Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln
 1 5 10 15
 Leu Met His Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile
 20 25 30

Tyr

<210> 56
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 56
 Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Pro Tyr Asp Val Pro Asp
 1 5 10 15
 Tyr Ala Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
 20 25 30

<210> 57
 <211> 1380
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(1353)

<400> 57
 atg ggg acc gcc cgg atc gca ccc ggc ctg gcg ctc ctg ctc tgc tgc 48
 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cat 96
 Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
 20 25 30

aat cgt ggc gga gga ggc gag gtg ttt gac cgc ctg ggc atg att tac	144
Asn Arg Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr	
35 40 45	
acc gtg ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc	192
Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu	
50 55 60	
atc ctg gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac	240
Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His	
65 70 75 80	
atg cac ctg ttc ctg tcc ttc atg ctg cgc gcc gtg agc atc ttc gtc	288
Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val	
85 90 95	
aag gac gct gtg ctc tac tct ggc gcc acg ctt gat gag gct gag cgc	336
Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg	
100 105 110	
ctc acc gag gag gag ctg cgc gcc atc gcc cag gcg ccc ccg ccg cct	384
Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro	
115 120 125	
gcc acc gcc gct gcc ggc tac gcg ggc tgc agg gtg gct gtg acc ttc	432
Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe	
130 135 140	
ttc ctt tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg	480
Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly	
145 150 155 160	
ctg tac ctg cac agc ctc atc ttc atg gcc ttc ttc tca gag aag aag	528
Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys	
165 170 175	
tac ctg tgg ggc ttc aca gtc ttc ggc tgg ggt ctg ccc gct gtc ttc	576
Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe	
180 185 190	
gtg gct gtg tgg gtc agt gtc aga gct acc ctg gcc aac acc ggg tgc	624
Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys	
195 200 205	
tgg gac ttg agc tcc ggg aac aaa aag tgg atc atc cag gtg ccc atc	672
Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile	
210 215 220	
ctg gcc tcc att gtg ctc aac ttc atc ctc ttc atc aat atc gtc cgg	720
Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg	
225 230 235 240	
gtg ctc gcc acc aag ctg cgg gag acc aac gcc ggc cgg tgt gac aca	768
Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr	
245 250 255	
cgg cag cag tac cgg aag ctg ctc aaa tcc acg ctg gtg ctc atg ccc	816
Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro	
260 265 270	
ctc ttt ggc gtc cac tac att gtc ttc atg gcc aca cca tac acc gag	864
Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu	

275	280	285	
gtc tca ggg acg ctc tgg caa gtc cag atg cac tat gag atg ctc ttc			912
Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe			
290	295	300	
aac tcc ttc cag gga ttt ttt gtc gca atc ata tac tgt ttc tgc aat			960
Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn			
305	310	315	320
ggc gag gta caa gct gag atc aag aaa tct tgg agc cgc tgg aca ctg			1008
Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu			
	325	330	335
gca ctg gac ttc aag cga aag gca cgc agc ggg agc agc agc tat agc			1056
Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser			
	340	345	350
tac ggc ccc atg gtg tcc cac aca agt gtg acc aat gtc ggc ccc cgt			1104
Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg			
	355	360	365
gtg gga ctc ggc ctg ccc ctc agc ccc cgc cta ctg ccc act gcc acc			1152
Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr			
	370	375	380
acc aac ggc cac cct cag ctg cct ggc cat gcc aag cca ggg acc cca			1200
Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro			
	385	390	395
gcc ctg gag acc ctc gag acc aca cca cct gcc atg gct gct ccc aag			1248
Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys			
	405	410	415
gac gat ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc			1296
Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala			
	420	425	430
tct ggg cct gag cgg cca cct gcc ctg cta cag gaa gag tgg gag aca			1344
Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr			
	435	440	445
gtc atg tga ccaggcgctg ggggctggac ctgctga			1380
Val Met			
450			

<210> 58

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 58

Met	Gly	Thr	Ala	Arg	Ile	Ala	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Cys	Cys
1				5			10						15		
Pro	Val	Leu	Ser	Ser	Ala	Tyr	Ala	Val	Ser	Glu	Ile	Gln	Leu	Met	His
		20				25						30			
Asn	Arg	Gly	Gly	Gly	Gly	Glu	Val	Phe	Asp	Arg	Leu	Gly	Met	Ile	Tyr

```
<210> 59
<211> 1380
<212> DNA
<213> Artificial Sequence
<220>
```

<220>

<223> Description of Artificial Sequence: modified PTH
receptor sequence

<220>

<221> CDS

<222> (28) .. (1335)

<400> 59

```

tggatccccgc ggccctaggc ggtggcgc atg ggg acc gcc cgg atc gca ccc ggc 54
                               Met Gly Thr Ala Arg Ile Ala Pro Gly
                               1                               5

ctg gcg ctc ctg ctc tgc tgc ccc gtg ctc agc tcc gca tat gag gtg 102
Leu Ala Leu Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Glu Val
10                               15                               20                               25

ttt gac cgc ctg ggc atg att tac acc gtg ggc tac tcc gtg tcc ctg 150
Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Val Ser Leu
                               30                               35                               40

gcg tcc ctc acc gta gct gtg ctc atc ctg gcc tac ttt agg cgg ctg 198
Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu
                               45                               50                               55

cac tgc acg cgc aac tac atc cac atg cac ctg ttc ctg tcc ttc atg 246
His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met
                               60                               65                               70

ctg cgc gcc gtg agc atc ttc gtc aag gac gct gtg ctc tac tct ggc 294
Leu Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly
75                               80                               85

gcc acg ctt gat gag gct gag cgc ctc acc gag gag gag ctg cgc gcc 342
Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu Arg Ala
90                               95                               100                               105

atc gcc cag gcg ccc ccg ccg cct gcc acc gcc gct gcc ggc tac gcg 390
Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr Ala Ala Ala Gly Tyr Ala
                               110                               115                               120

ggc tgc agg gtg gct gtg acc ttc ttc ctt tac ttc ctg gcc acc aac 438
Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn
                               125                               130                               135

tac tac tgg att ctg gtg gag ggg ctg tac ctg cac agc ctc atc ttc 486
Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe
140                               145                               150

atg gcc ttc ttc tca gag aag aag tac ctg tgg ggc ttc aca gtc ttc 534
Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Val Phe
155                               160                               165

ggc tgg ggt ctg ccc gct gtc ttc gtg gct gtg tgg gtc agt gtc aga 582
Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Ser Val Arg
170                               175                               180                               185

gct acc ctg gcc aac acc ggg tgc tgg gac ttg agc tcc ggg aac aaa 630
Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser Gly Asn Lys
                               190                               195                               200

aag tgg atc atc cag gtg ccc atc ctg gcc tcc att gtg ctc aac ttc 678
Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Leu Asn Phe

```

205										210										215										
atc	ctc	ttc	atc	aat	atc	gtc	cgg	gtg	ctc	gcc	acc	aag	ctg	cgg	gag	726														
Ile	Leu	Phe	Ile	Asn	Ile	Val	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu															
		220						225					230																	
acc	aac	gcc	ggc	cgg	tgt	gac	aca	cgg	cag	cag	tac	cgg	aag	ctg	ctc	774														
Thr	Asn	Ala	Gly	Arg	Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu															
		235					240					245																		
aaa	tcc	acg	ctg	gtg	ctc	atg	ccc	ctc	ttt	ggc	gtc	cac	tac	att	gtc	822														
Lys	Ser	Thr	Leu	Val	Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile	Val															
		250				255					260				265															
ttc	atg	gcc	aca	cca	tac	acc	gag	gtc	tca	ggg	acg	ctc	tgg	caa	gtc	870														
Phe	Met	Ala	Thr	Pro	Tyr	Thr	Glu	Val	Ser	Gly	Thr	Leu	Trp	Gln	Val															
				270					275					280																
cag	atg	cac	tat	gag	atg	ctc	ttc	aac	tcc	ttc	cag	gga	ttt	ttt	gtc	918														
Gln	Met	His	Tyr	Glu	Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val															
			285					290					295																	
gca	atc	ata	tac	tgt	ttc	tgc	aat	ggc	gag	gta	caa	gct	gag	atc	aag	966														
Ala	Ile	Ile	Tyr	Cys	Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys															
		300					305					310																		
aaa	tct	tgg	agc	cgc	tgg	aca	ctg	gca	ctg	gac	ttc	aag	cga	aag	gca	1014														
Lys	Ser	Trp	Ser	Arg	Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala															
		315				320					325																			
cgc	agc	ggg	agc	agc	agc	tat	agc	tac	ggc	ccc	atg	gtg	tcc	cac	aca	1062														
Arg	Ser	Gly	Ser	Ser	Ser	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr															
		330				335				340					345															
agt	gtg	acc	aat	gtc	ggc	ccc	cgt	gtg	gga	ctc	ggc	ctg	ccc	ctc	agc	1110														
Ser	Val	Thr	Asn	Val	Gly	Pro	Arg	Val	Gly	Leu	Gly	Leu	Pro	Leu	Ser															
				350					355					360																
ccc	cgc	cta	ctg	ccc	act	gcc	acc	acc	aac	ggc	cac	cct	cag	ctg	cct	1158														
Pro	Arg	Leu	Leu	Pro	Thr	Ala	Thr	Thr	Asn	Gly	His	Pro	Gln	Leu	Pro															
			365					370					375																	
ggc	cat	gcc	aag	cca	ggg	acc	cca	gcc	ctg	gag	acc	ctc	gag	acc	aca	1206														
Gly	His	Ala	Lys	Pro	Gly	Thr	Pro	Ala	Leu	Glu	Thr	Leu	Glu	Thr	Thr															
		380					385					390																		
cca	cct	gcc	atg	gct	gct	ccc	aag	gac	gat	ggg	ttc	ctc	aac	ggc	tcc	1254														
Pro	Pro	Ala	Met	Ala	Ala	Pro	Lys	Asp	Asp	Gly	Phe	Leu	Asn	Gly	Ser															
		395				400					405																			
tgc	tca	ggc	ctg	gac	gag	gag	gcc	tct	ggg	cct	gag	cgg	cca	cct	gcc	1302														
Cys	Ser	Gly	Leu	Asp	Glu	Glu	Ala	Ser	Gly	Pro	Glu	Arg	Pro	Pro	Ala															
		410			415				420						425															
ctg	cta	cag	gaa	gag	tgg	gag	aca	gtc	atg	tga	ccaggcgctg	ggggctggac	1355																	
Leu	Leu	Gln	Glu	Glu	Trp	Glu	Thr	Val	Met																					
				430				435																						
ctgctgacat	agtggaatgga	cagat														1380														

<211> 435
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 60
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
1 5 10 15
Pro Val Leu Ser Ser Ala Tyr Glu Val Phe Asp Arg Leu Gly Met Ile
20 25 30
Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val
35 40 45
Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile
50 55 60
His Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe
65 70 75 80
Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu
85 90 95
Arg Leu Thr Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro
100 105 110
Pro Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr
115 120 125
Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu
130 135 140
Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys
145 150 155 160
Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val
165 170 175
Phe Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly
180 185 190
Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro
195 200 205
Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val
210 215 220
Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp
225 230 235 240
Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met
245 250 255
Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr
260 265 270
Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu
275 280 285
Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys
290 295 300
Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr
305 310 315 320
Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr
325 330 335
Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro
340 345 350
Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala
355 360 365
Thr Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr
370 375 380
Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro
385 390 395 400
Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu
405 410 415

Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu
 420 425 430
 Thr Val Met
 435

<210> 61
 <211> 1363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(1347)

<400> 61
 atg ggg acc gcc cgg atc gca ccc ggc ctg gcg ctc ctg ctc tgc tgc 48
 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cac 96
 Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
 20 25 30
 ggc gga gga ggc gag gtg ttt gac cgc ctg ggc atg att tac acc gtg 144
 Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val
 35 40 45
 ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc atc ctg 192
 Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu
 50 55 60
 gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac 240
 Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His
 65 70 75 80
 ctg ttc ctg tcc ttc atg ctg cgc gcc gtg agc atc ttc gtc aag gac 288
 Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp
 85 90 95
 gct gtg ctc tac tct ggc gcc acg ctt gat gag gct gag cgc ctc acc 336
 Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr
 100 105 110
 gag gag gag ctg cgc gcc atc gcc cag gcg ccc ccg ccg cct gcc acc 384
 Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr
 115 120 125
 gcc gct gcc ggc tac gcg ggc tgc agg gtg gct gtg acc ttc ttc ctt 432
 Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu
 130 135 140
 tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg ctg tac 480
 Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr
 145 150 155 160
 ctg cac agc ctc atc ttc atg gcc ttc ttc tca gag aag aag tac ctg 528

Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	Glu	Lys	Lys	Tyr	Leu		
				165					170						175		
tgg	ggc	ttc	aca	gtc	ttc	ggc	tgg	ggt	ctg	ccc	gct	gtc	ttc	gtg	gct	576	
Trp	Gly	Phe	Thr	Val	Phe	Gly	Trp	Gly	Leu	Pro	Ala	Val	Phe	Val	Ala		
			180					185					190				
gtg	tgg	gtc	agt	gtc	aga	gct	acc	ctg	gcc	aac	acc	ggg	tgc	tgg	gac	624	
Val	Trp	Val	Ser	Val	Arg	Ala	Thr	Leu	Ala	Asn	Thr	Gly	Cys	Trp	Asp		
			195				200					205					
ttg	agc	tcc	ggg	aac	aaa	aag	tgg	atc	atc	cag	gtg	ccc	atc	ctg	gcc	672	
Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	Val	Pro	Ile	Leu	Ala		
	210					215					220						
tcc	att	gtg	ctc	aac	ttc	atc	ctc	ttc	atc	aac	atc	gtc	cgg	gtg	ctc	720	
Ser	Ile	Val	Leu	Asn	Phe	Ile	Leu	Phe	Ile	Asn	Ile	Val	Arg	Val	Leu		
225					230					235					240		
gcc	acc	aag	ctg	cgg	gag	acc	aac	gcc	ggc	cgg	tgt	gac	aca	cgg	cag	768	
Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	Cys	Asp	Thr	Arg	Gln		
				245					250					255			
cag	tac	cgg	aag	ctg	ctc	aaa	tcc	acg	ctg	gtg	ctc	atg	ccc	ctc	ttt	816	
Gln	Tyr	Arg	Lys	Leu	Leu	Lys	Ser	Thr	Leu	Val	Leu	Met	Pro	Leu	Phe		
			260					265					270				
ggc	gtc	cac	tac	att	gtc	ttc	atg	gcc	aca	cca	tac	acc	gag	gtc	tca	864	
Gly	Val	His	Tyr	Ile	Val	Phe	Met	Ala	Thr	Pro	Tyr	Thr	Glu	Val	Ser		
		275					280					285					
ggg	acg	ctc	tgg	caa	gtc	cag	atg	cac	tat	gag	atg	ctc	ttc	aac	tcc	912	
Gly	Thr	Leu	Trp	Gln	Val	Gln	Met	His	Tyr	Glu	Met	Leu	Phe	Asn	Ser		
	290					295					300						
ttc	cag	gga	ttt	ttt	gtc	gca	atc	ata	tac	tgt	ttc	tgc	aac	ggc	gag	960	
Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	Phe	Cys	Asn	Gly	Glu		
305					310					315					320		
gta	caa	gct	gag	atc	aag	aaa	tct	tgg	agc	cgc	tgg	aca	ctg	gca	ctg	1008	
Val	Gln	Ala	Glu	Ile	Lys	Lys	Ser	Trp	Ser	Arg	Trp	Thr	Leu	Ala	Leu		
				325					330					335			
gac	ttc	aag	cga	aag	gca	cgc	agc	ggg	agc	agc	agc	tat	agc	tac	ggc	1056	
Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	Ser	Tyr	Ser	Tyr	Gly		
			340					345					350				
ccc	atg	gtg	tcc	cac	aca	agt	gtg	acc	aac	gtc	ggc	ccc	cgt	gtg	gga	1104	
Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	Gly	Pro	Arg	Val	Gly		
			355				360					365					
ctc	ggc	ctg	ccc	ctc	agc	ccc	cgc	cta	ctg	ccc	act	gcc	acc	acc	aac	1152	
Leu	Gly	Leu	Pro	Leu	Ser	Pro	Arg	Leu	Leu	Pro	Thr	Ala	Thr	Thr	Asn		
	370					375					380						
ggc	cac	cct	cag	ctg	cct	ggc	cat	gcc	aag	cca	ggg	acc	cca	gcc	ctg	1200	
Gly	His	Pro	Gln	Leu	Pro	Gly	His	Ala	Lys	Pro	Gly	Thr	Pro	Ala	Leu		
	385				390				395						400		
gag	acc	ctc	gag	acc	aca	cca	cct	gcc	atg	gct	gct	ccc	aag	gac	gat	1248	
Glu	Thr	Leu	Glu	Thr	Thr	Pro	Pro	Ala	Met	Ala	Ala	Pro	Lys	Asp	Asp		
				405				410						415			

```

ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc tct ggg      1296
Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly
               420                     425                     430

cct gag cgg cca cct gcc ctg cta cag gaa gag tgg gag aca gtc atg      1344
Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met
               435                     440                     445

tga ccaggcgctg ggggct                                              1363

```

<210> 62
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

```

<400> 62
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1               5               10               15
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
               20               25               30
Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val
               35               40               45
Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu
 50               55               60
Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His
 65               70               75               80
Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp
               85               90               95
Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr
 100              105              110
Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr
 115              120              125
Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu
 130              135              140
Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr
 145              150              155              160
Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu
               165              170              175
Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala
 180              185              190
Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp
 195              200              205
Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala
 210              215              220
Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu
 225              230              235              240
Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln
               245              250              255
Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe
 260              265              270
Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser
 275              280              285
Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser
 290              295              300
Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu
 305              310              315              320

```



```

Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu
              325              330              335
Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly
              340              345              350
Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly
              355              360              365
Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn
              370              375              380
Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu
385              390              395              400
Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp
              405              410              415
Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly
              420              425              430
Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met
              435              440              445

```

<210> 63
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 63
 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
 1 5 10 15

<210> 64
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 64
 Ala Val Ser Glu His Gln Leu Leu His Gly Gly Gly Gly Gly Ile Gln
 1 5 10 15
 Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
 20 25 30

<210> 65
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 65
 Ala Val Ser Glu His Gly Gly Gly Gly Gly Gly Gly Gly Gly Ile Gln
 1 5 10 15
 Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
 20 25 30

<210> 66
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 66
Ala Val Ser Glu His Gln Leu Leu His Gly Gly Gly Gly Gly Gly Gly
1 5 10 15
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
20 25 30

<210> 67
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 67

Ala Val Ser Glu Ile Gln Leu Met His Asn Leu
1 5 10

<210> 68
<211> 99
<212> DNA
<213> Artificial sequence

<220>
<223> modified PTH sequence

<400> 68
ctctgctgcc ccgtgctcag ctccgcgtac gcggtttccg aaatccagct gatgcacggc 60
ggaggaggcg aggtgtttga ccgcctgggc atgatttac 99

<210> 69
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> modified PTH receptor sequence

<220>
<221> CDS
<222> (3)..(47)

<400> 69
cc gaa atc cag ctg atg cat aat cgt ggc gga gga ggc gag gtg ttt g 48

Glu Ile Gln Leu Met His Asn Arg Gly Gly Gly Gly Glu Val Phe
1 5 10 15

<210> 70
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> modified PTH receptor sequence

<400> 70

Glu Ile Gln Leu Met His Asn Arg Gly Gly Gly Gly Glu Val Phe Asp
1 5 10 15

<210> 71
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 71

Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 72
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> modified PTH receptor sequence

<400> 72

Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly
1 5 10

<210> 73
<211> 14
<212> PRT
<213> Homo sapiens

<400> 73

Ala Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His
1 5 10

β^s
<210> 74
<211> 9
<212> PRT
<213> Rattus sp.

<400> 74
Ala Val Ser Glu Ile Gln Leu Met His
1 5
